AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of the claims in the application:

Listing of Claims:

1. (currently amended) A method for amplifying expressed genetic sequences from genomic DNA (gDNA) [[gDNA]] selected from a higher-order eukaryotic species, for printing on DNA microarrays, wherein the method comprises:

identifying a 3' untranslated region (3'UTR) ~~either 1) a 3'UTR~~ of a gDNA sequence based on the presence of a stop codon and a polyadenylation signal in the gDNA sequence ~~corresponding to an expressed mRNA sequence, or 2) an exon of a gene defined by computer software~~;

selecting a predetermined gDNA sequence within the 3'UTR ~~or exon~~;

designing a probe for said predetermined gDNA sequence;

performing a first polymerase chain reaction (PCR) for the 3'UTR ~~or exon~~ on gDNA to generate PCR-product;

separating the resultant PCR-product by a size-differentiation process selected from the group consisting of electrophoresis and chromatography;

selecting a predetermined band from the size-differentiated samples; [[and]]

performing a second polymerase chain reaction to amplify a PCR product in the predetermined band ~~predetermined sequence~~; and

depositing a sequence amplified by said second polymerase chain reaction to a substrate of an array.

2. (currently amended) The method according to claim 1, wherein a plurality of said ~~final~~ amplified sequences are deposited on a substrate in an array.

3. (currently amended) The method according to claim 1, wherein said amplified sequence is ~~final amplified sequences are~~ the sequence of one exon and contains no polyadenosine.

4. (currently amended) The method according to claim 1, wherein said predetermined gDNA sequence within the 3'UTR ~~or exon~~ is selected by use of computer software.

5. (currently amended) The method according to claim 1, wherein said selected predetermined gDNA sequence within the 3'UTR ~~or exon~~ has a length of at least about 75 nucleotides.

6. (original) The method according to claim 5, wherein said selected predetermined gDNA sequence has a length of about 200 to about 600 bases.

7. (original) The method according to claim 6, wherein said selected predetermined gDNA sequence has a length of about 250 to about 450 bases.

8. (original) The method according to claim 1, wherein said selected predetermined gDNA sequence has an overall homology of less than or equal to about 70% to any other genomic sequence in the same genome.

9. (original) The method according to claim 8, wherein said selected predetermined gDNA sequence has an overall homology of less than or equal to about 40% to any other genomic sequence in the same genome.

10. (original) The method according to claim 8, wherein said selected predetermined gDNA sequence has an overall homology of from about 20% to 30% to any other genomic sequence in the same genome.

11. (currently amended) The method according to claim 1, wherein ~~said method can generate PCR products that contain~~ said amplified sequence contains over 90 percent correct predetermined sequence.

12. (currently amended) The method according to claim 1, wherein said array has [[is]] a rectilinear format.

13-26. (canceled)

27. (currently amended) The method according to claim 1, wherein said predetermined gDNA sequence within the 3'UTR ~~or exon~~ has a length of up to about 2000 nucleotides.

28. (new) A method for amplifying expressed genetic sequences from genomic DNA (gDNA) selected from a higher-order eukaryotic species, for printing on DNA microarrays, wherein the method comprises:

identifying an exon of a gene defined by computer software;

selecting a predetermined gDNA sequence within the exon;

designing a probe for said predetermined gDNA sequence;

performing a first polymerase chain reaction (PCR) for the exon on gDNA to generate PCR-product;

separating the resultant PCR-product by a size-differentiation process selected from the group consisting of electrophoresis and chromatography;

selecting a predetermined band from the size-differentiated samples;

performing a second PCR to amplify a product in the predetermined band; and

depositing a sequence amplified by said second PCR to a substrate of an array

29. (new) A method for making a DNA array, comprising:

performing a first PCR to amplify a 3'UTR, or a segment thereof, in a gDNA of a higher-order eukaryotic species;

separating products of said first PCR to select a product with a predetermined size;

performing a second PCR to amplify a sequence in said selected product; and

depositing said amplified sequence to a substrate of the DNA array.

30. (new) The method of claim 29, comprising:

performing PCRs to amply a plurality of 3'UTRs, or segments thereof, in genomic DNAs of said higher-order eukaryotic species;

separating products of said PCRs to select products with predetermined sizes;

performing PCRs to amplify sequences in said selected products; and

depositing said amplified sequences to the DNA array.

31. (new) The method of claim 30, wherein each said 3'UTR is located between a stop codon and a polyadenylation signal of a different respective gene.

32. (new) The method of claim 31, wherein each said 3'UTR or segment comprises from about 75 to about 2,000 nucleotides, and each said separating step is accomplished by electrophoresis or chromatography.

33. (new) The method of claim 31, wherein said higher-order eukaryotic species is a mammal, and each said 3'UTR or segment has an overall homology of no more than about 40% to any other genomic sequence in the genome of said mammal.

34. (new) The method of claim 29, wherein said first and second PCRs are performed using the same pair of primers.